

Fig. 1

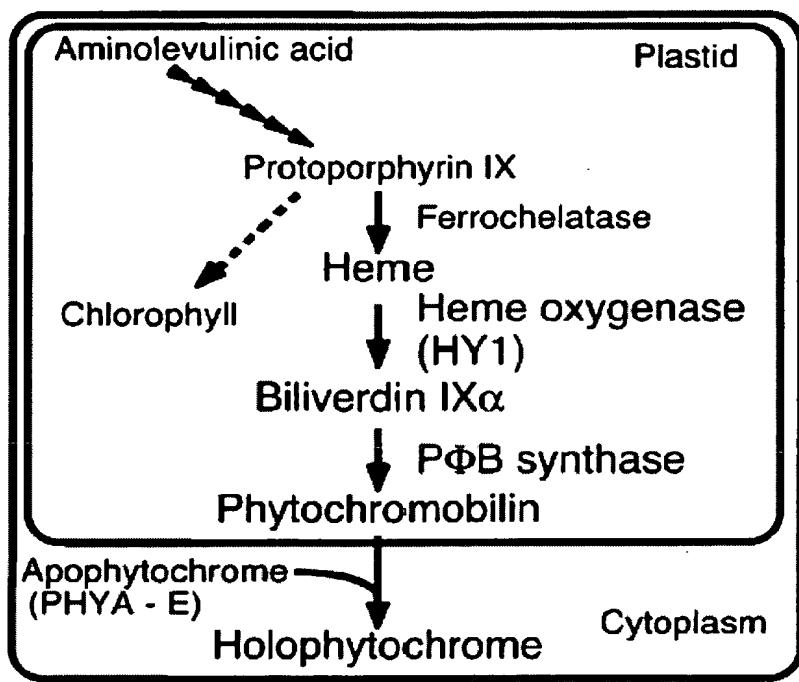


Fig. 2

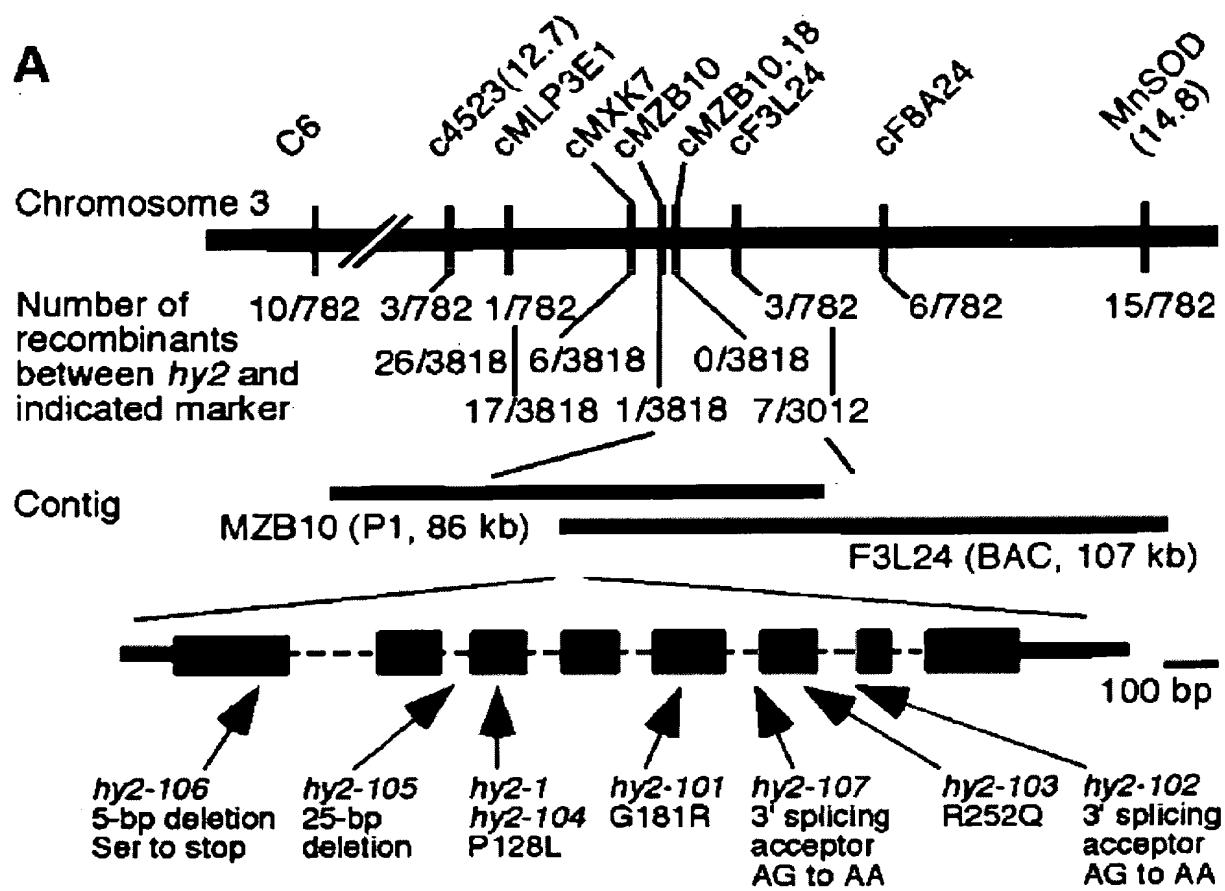


Fig. 3A

Fig. 3B

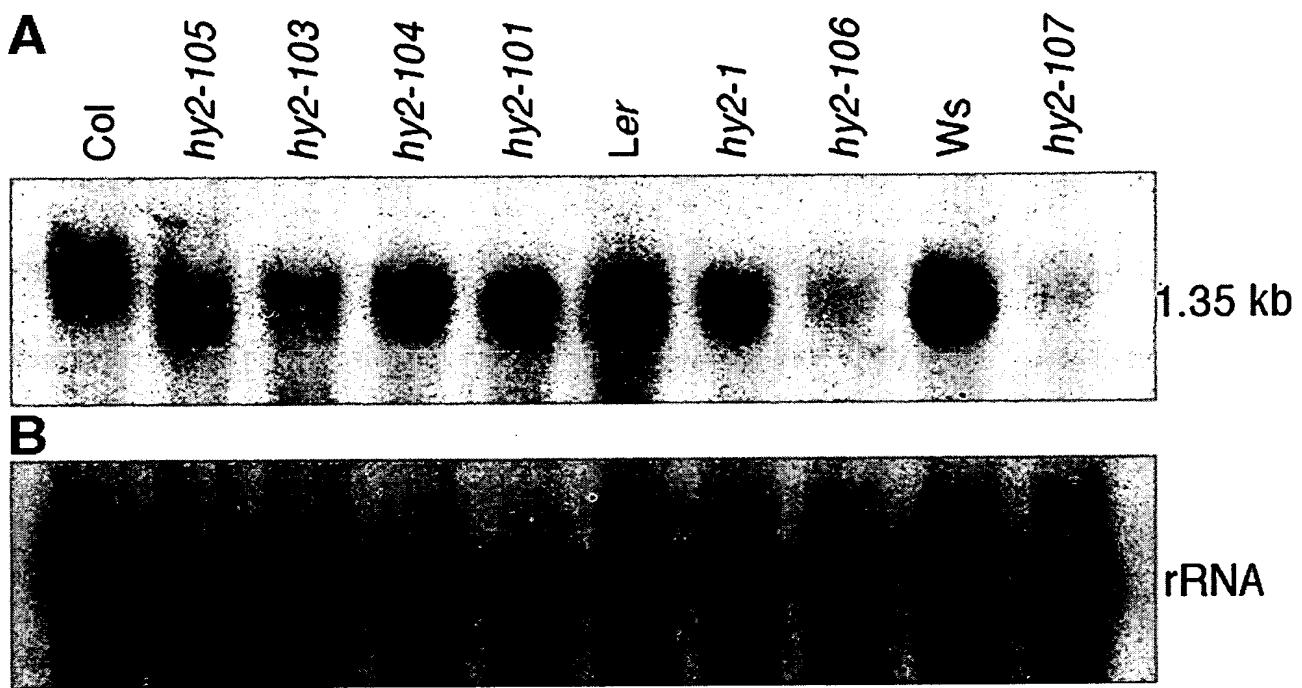


Fig. 4A and Fig. 4B

Fig. 5

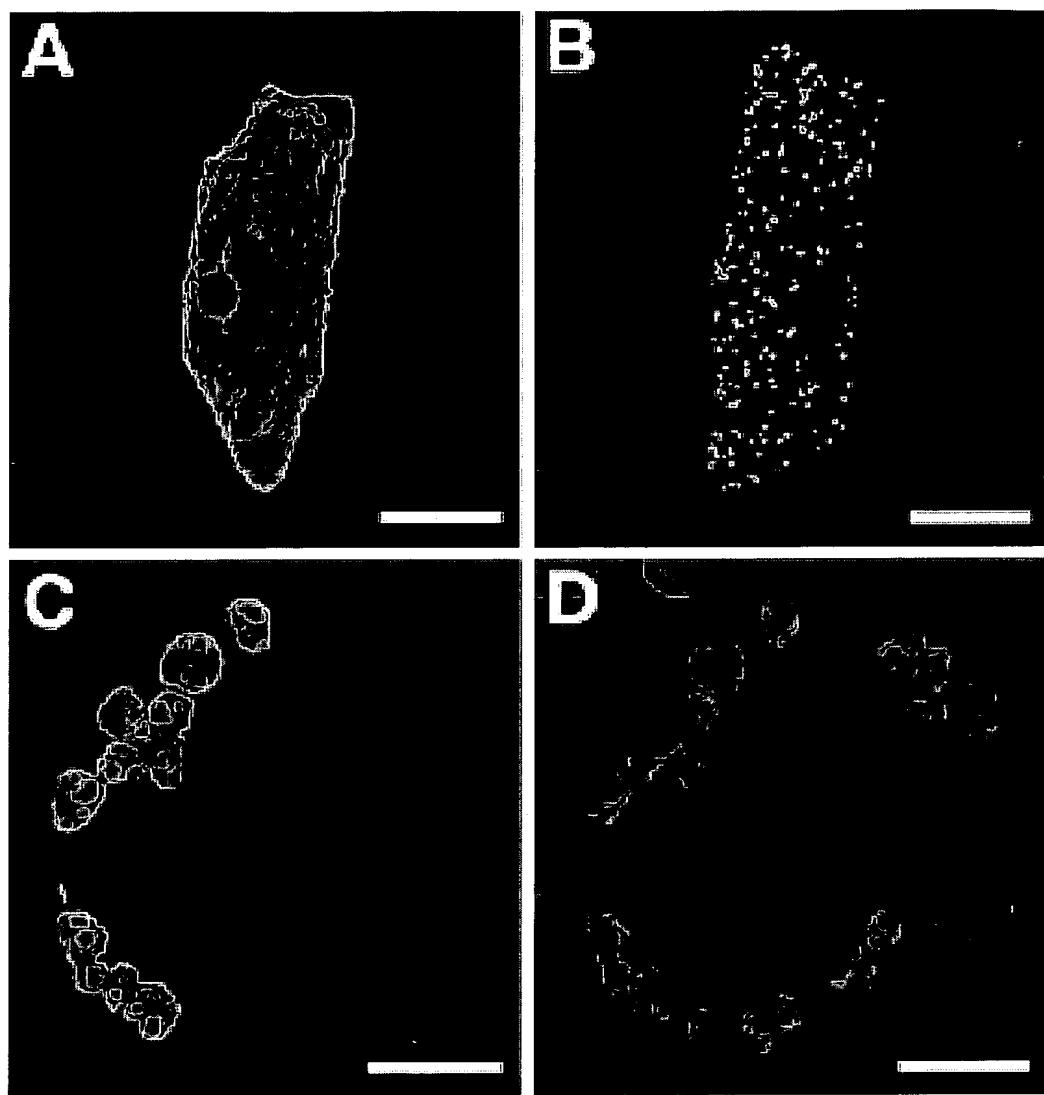


Fig. 6A - 6D

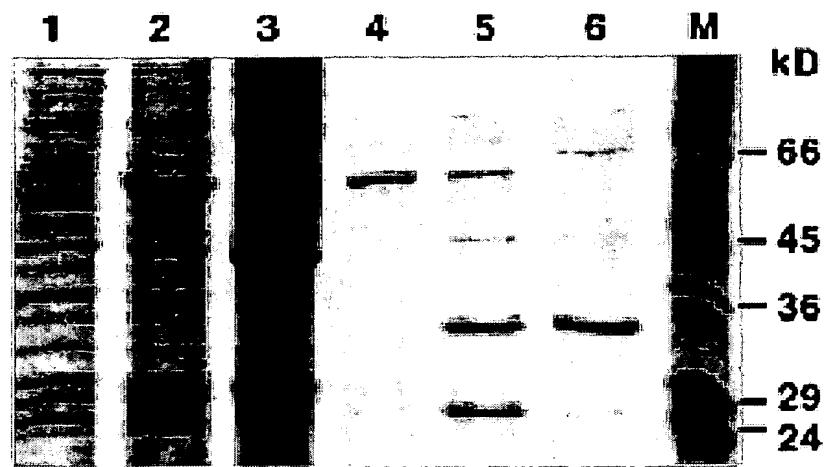


Fig. 7

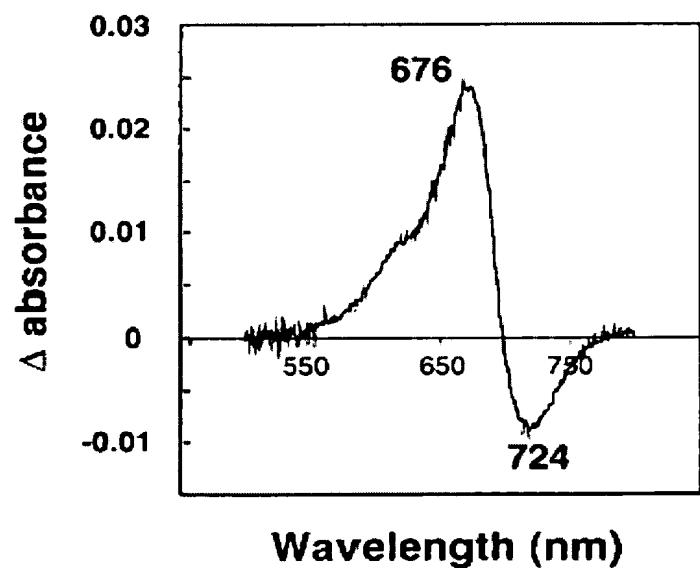


Fig. 8

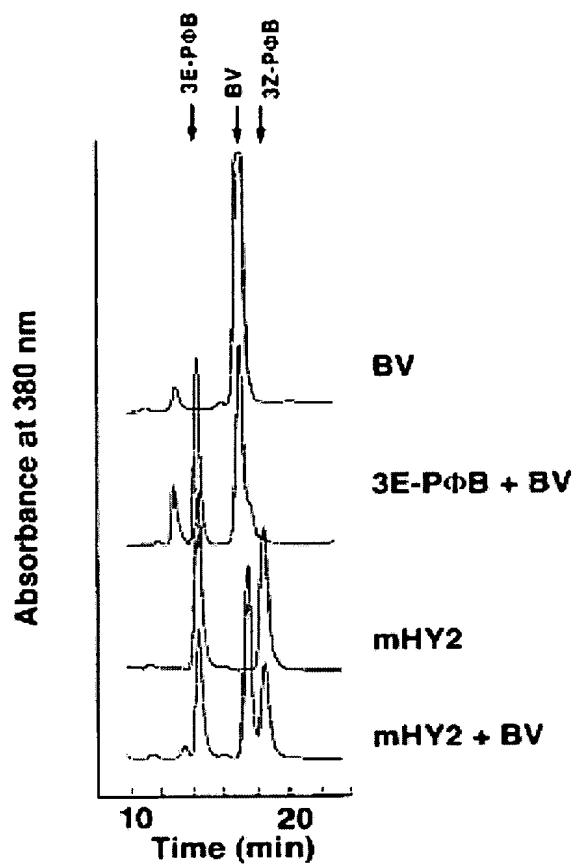


Fig. 9

PCY1_ANASP	*	200	*	220	*	240	*	260
PCY1_NOSPU	:	PESYNTAIAQQPV	--	LNPSQPRPLP	WGN1	--	SSPEEBAM	FLGVRUREP
PCY1_SYN1	:	PESYNTAIAQQQ	--	LNPSQPRPLP	WGN1	--	GSPEEBAM	FLSRRVREF
PCY1_SYN81	:	PAAYOKSIAEYZQ	--	PEFEQORELPPWGE	I	--	GSPEEBAM	FLHCNQA
PCY1_PRIME	:	PSGIETTAAGTSPS	--	PAFRQVRDILPGWGT	I	--	SNVTEER	FLQVVD
PCY1_SHIDK	--	SVFKSKREIPIWGN	I	--	FSKVNFEASL	--	DGAEEBVL	FRSREEV
PeBa_SYN1	:	LDRYFSGKEELNQRF	PDLN	GEETMRSFDPNQY	--	FSWVLLFCRG	--	KNESEKNA
PeBa_SYN81	:	LDRHFDGKDLNARF	PDLN	GEETMRSFDPNQY	--	FSWVLLFCRG	--	FCCKIVDNY
PeBa_PR0MA	:	FCRYYKDIQIKRN	RFVDFNSQ	KTMKIYDSNKY	--	FSPWVLLNG	--	SPDSDYEI
PeBa_PR0ME	:	LQKYCSS1DFIKNQY	SVDN	NKMKIYDSKKY	--	FSPWVMICRG	--	SPKAFSA
PeBa_NOSPU	:	QNKYIAPIKYTHN	KY	PDLAQNL	EMKTYDANOY	--	GAEQADLSEL	PKAFSA
PeBa_SYN1	:	THWMDRIPIFERW	RDQL	PGGQPIPEAQP	F	--	GSEBADRSEL	PKAFSA
PeBa_SYN81	:	TQPVNWRIMPFLPER	WQAE	LPDGQPIPEAQP	Y	--	SFDLQCS	TEAKILDEFI
PeBa_PR0MA	:	TENVWPRIPIDH	HWQSL	PGGCEIPKEAQP	Y	--	NKLNLDRDLE	NNIFCS
PeBa_PR0ME	:	NSLEQI	KTKS	SSSLPV	AEKNSEDWAKE	--	QNLIFCS	ENMLTINKLH
PeBa_NOSPU	:	QAKYTXEPILP	ITPAH	QHQLSWGGDF	PERAQP	--	-QNLIFCS	ENMLTINKLH
HY2_ARATH	:	QDKYNNKIMSIY	H	KYAE	TPWGGKLTGSE	SIKE	-DAETV	STRVEAFQDY
RCCR_ARATH	:	LKEYQDTALDSB	RSO	LLPEVNPYVPSL	EVRSAFS	BTASMLKIDAE	--	EGDELLIE
RCCR_HORVU	:	IEKMYDTEV	DQKR	QIIEQLPQAR	YPSL	EV	ERV	FLPQF
4								
PCY1_ANASP	*	280	*	300	*	320	*	340
PCY1_NOSPU	:	QO1IA-G	CHNYCSKQQQN	D	KTRRVIDEKA	FGJD	WAEN	YMTVLE
PCY1_SYN1	:	TON1A-G	CHNYC	TQOQN	D	KTRRVIDEKA	FGJ	VAEN
PCY1_SYN81	:	LEH1RQ-G	CHY	QQQQ	QKN	D	EN	YMTVLE
PCY1_PR0ME	:	IRR1E	G	SYL	C	D	FLD	FLD
PeBa_SYN1	:	IEER1N	Y	CKNYC	VQ	D	FLD	FLD
PeBa_PR0MA	:	PEBVKNL	CDK	Y	QNS	D	FLP	FLP
PeBa_SYN81	:	PGDVERL	QNAYD	VSAER	D	PAHGLFT	SHF	QSPA
PeBa_PR0MA	:	PSKVEQLH	IN	YSAER	D	PAHGLFT	SHF	QSPA
PeBa_PR0ME	:	LEQ1KNN	QIDYD	KNSAED	D	PAHGLFT	SHF	QSPA
PeBa_NOSPU	:	IQR1VKACKD	YDQ	YSAEDR	D	PAHGLFT	SHF	QSPA
PeBa_SYN1	:	EVL1EQ	-	DYRAEKD	D	PAHGLFT	SHF	QSPA
PeBa_SYN81	:	EL1ES	-	GCCKRYTA	D	PAHGLFT	SHF	QSPA
PeBa_PR0MA	:	1K1LE	-	GCCKAYTIN	D	PAHGLFT	SHF	QSPA
PeBa_PR0ME	:	QEL1N	-	GNDYLN	D	PAHGLFT	SHF	QSPA
PeBa_NOSPU	:	IV1A	Q	RAO	D	PAHGLFT	SHF	QSPA
HY2_ARATH	:	VR1ANCE	A	CHY	D	PAHGLFT	SHF	QSPA
RCCR_ARATH	:	ERME1LER	RDK	SER	D	PAHGLFT	SHF	QSPA
RCCR_HORVU	:	ERE1MV	KRDR	TVRSKS	D	PAHGLFT	SHF	QSPA
4								
PCY1_ANASP	*	290	*	310	*	330	*	350
PCY1_NOSPU	:	QO1IA-G	CHNYCSKQQQN	D	KTRRVIDEKA	FGJD	WAEN	YMTVLE
PCY1_SYN1	:	TON1A-G	CHNYC	TQOQN	D	KTRRVIDEKA	FGJ	VAEN
PCY1_SYN81	:	LEH1RQ-G	CHY	QQQQ	QKN	D	EN	YMTVLE
PCY1_PR0ME	:	IRR1E	G	SYL	C	D	FLD	FLD
PeBa_SYN1	:	IEER1N	Y	CKNYC	VQ	D	FLP	FLP
PeBa_PR0MA	:	PEBVKNL	CDK	Y	QNS	D	FLP	FLP
PeBa_SYN81	:	PGDVERL	QNAYD	VSAER	D	PAHGLFT	SHF	QSPA
PeBa_PR0MA	:	PSKVEQLH	IN	YSAER	D	PAHGLFT	SHF	QSPA
PeBa_PR0ME	:	LEQ1KNN	QIDYD	KNSAED	D	PAHGLFT	SHF	QSPA
PeBa_NOSPU	:	IQR1VKACKD	YDQ	YSAEDR	D	PAHGLFT	SHF	QSPA
PeBa_SYN1	:	EVL1EQ	-	DYRAEKD	D	PAHGLFT	SHF	QSPA
PeBa_SYN81	:	EL1ES	-	GCCKRYTA	D	PAHGLFT	SHF	QSPA
PeBa_PR0MA	:	1K1LE	-	GCCKAYTIN	D	PAHGLFT	SHF	QSPA
PeBa_PR0ME	:	QEL1N	-	GNDYLN	D	PAHGLFT	SHF	QSPA
PeBa_NOSPU	:	IV1A	Q	RAO	D	PAHGLFT	SHF	QSPA
HY2_ARATH	:	VR1ANCE	A	CHY	D	PAHGLFT	SHF	QSPA
RCCR_ARATH	:	ERME1LER	RDK	SER	D	PAHGLFT	SHF	QSPA
RCCR_HORVU	:	ERE1MV	KRDR	TVRSKS	D	PAHGLFT	SHF	QSPA
4								
PCY1_ANASP	*	300	*	320	*	340	*	360
PCY1_NOSPU	:	QO1IA-G	CHNYCSKQQQN	D	KTRRVIDEKA	FGJD	WAEN	YMTVLE
PCY1_SYN1	:	TON1A-G	CHNYC	TQOQN	D	KTRRVIDEKA	FGJ	VAEN
PCY1_SYN81	:	LEH1RQ-G	CHY	QQQQ	QKN	D	EN	YMTVLE
PCY1_PR0ME	:	IRR1E	G	SYL	C	D	FLD	FLD
PeBa_SYN1	:	IEER1N	Y	CKNYC	VQ	D	FLP	FLP
PeBa_PR0MA	:	PEBVKNL	CDK	Y	QNS	D	FLP	FLP
PeBa_SYN81	:	PGDVERL	QNAYD	VSAER	D	PAHGLFT	SHF	QSPA
PeBa_PR0MA	:	PSKVEQLH	IN	YSAER	D	PAHGLFT	SHF	QSPA
PeBa_PR0ME	:	LEQ1KNN	QIDYD	KNSAED	D	PAHGLFT	SHF	QSPA
PeBa_NOSPU	:	IQR1VKACKD	YDQ	YSAEDR	D	PAHGLFT	SHF	QSPA
PeBa_SYN1	:	EVL1EQ	-	DYRAEKD	D	PAHGLFT	SHF	QSPA
PeBa_SYN81	:	EL1ES	-	GCCKRYTA	D	PAHGLFT	SHF	QSPA
PeBa_PR0MA	:	1K1LE	-	GCCKAYTIN	D	PAHGLFT	SHF	QSPA
PeBa_PR0ME	:	QEL1N	-	GNDYLN	D	PAHGLFT	SHF	QSPA
PeBa_NOSPU	:	IV1A	Q	RAO	D	PAHGLFT	SHF	QSPA
HY2_ARATH	:	VR1ANCE	A	CHY	D	PAHGLFT	SHF	QSPA
RCCR_ARATH	:	ERME1LER	RDK	SER	D	PAHGLFT	SHF	QSPA
RCCR_HORVU	:	ERE1MV	KRDR	TVRSKS	D	PAHGLFT	SHF	QSPA
4								

Fig. 10 cont'd

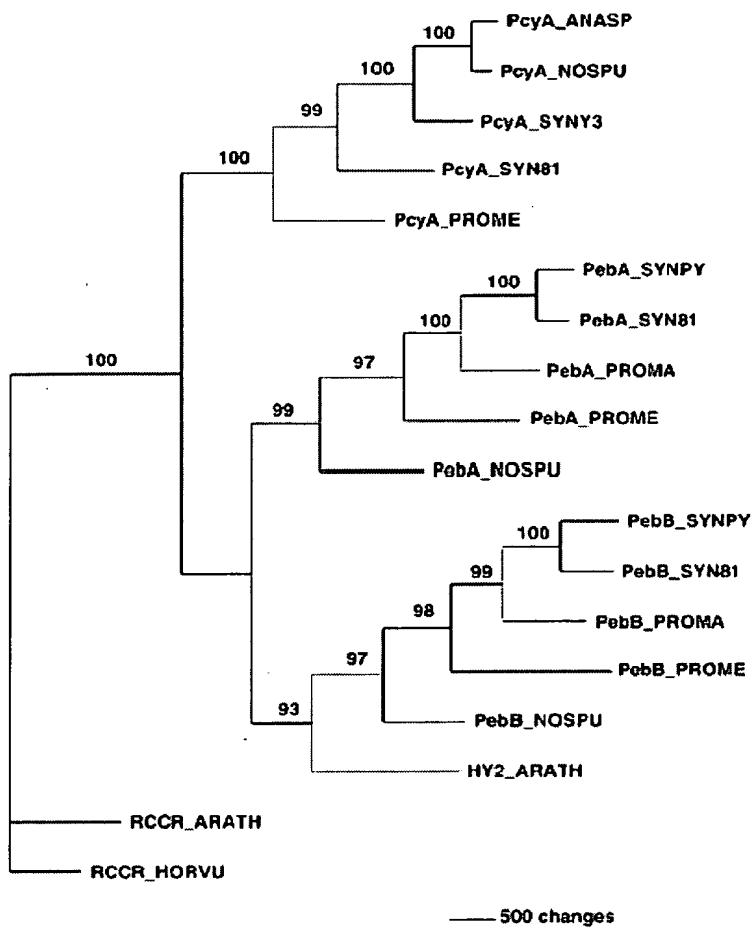


Fig. 11

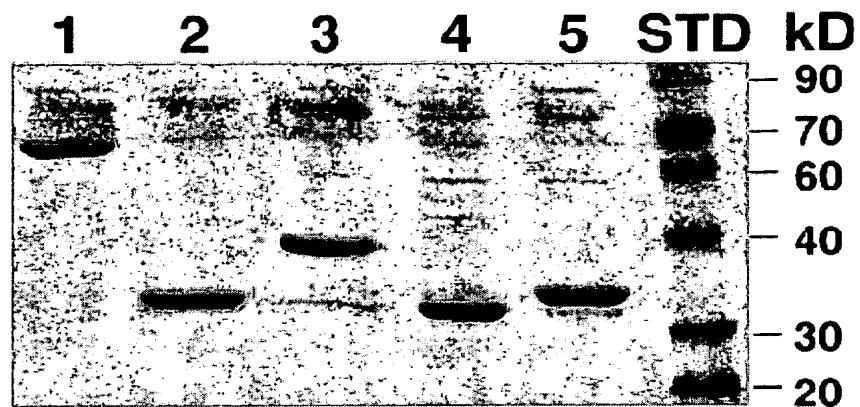


Fig. 12

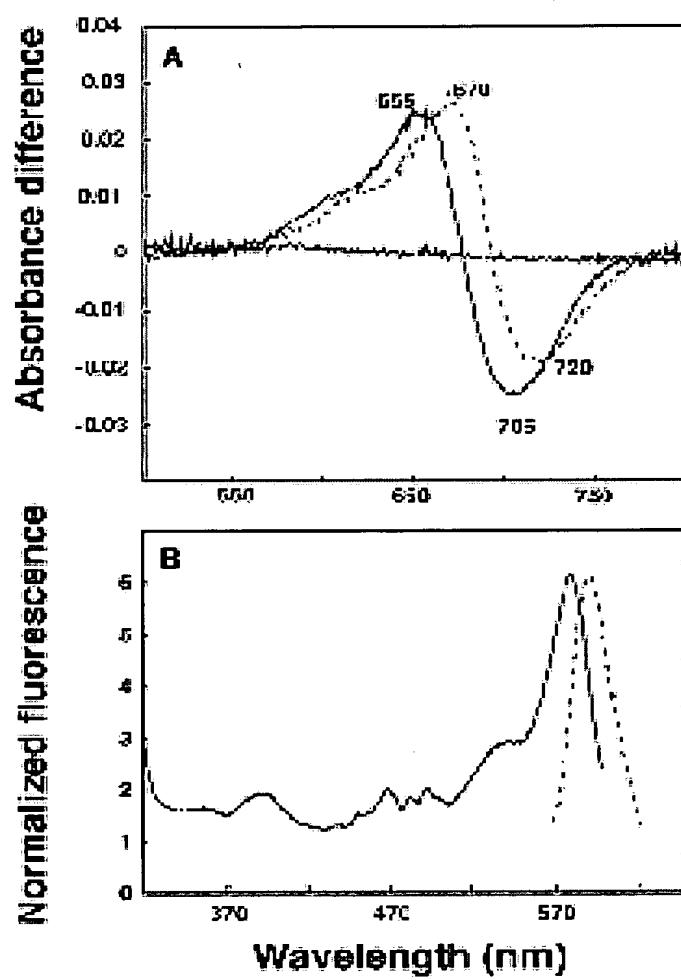


Fig. 13A and 13B

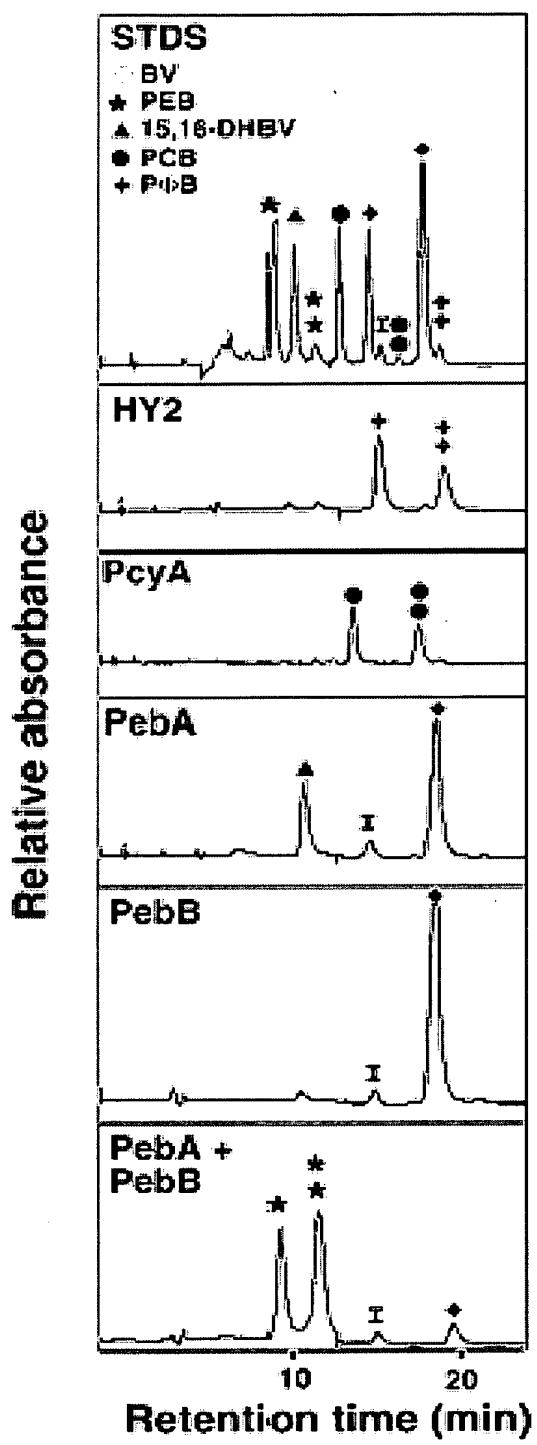


Fig. 14

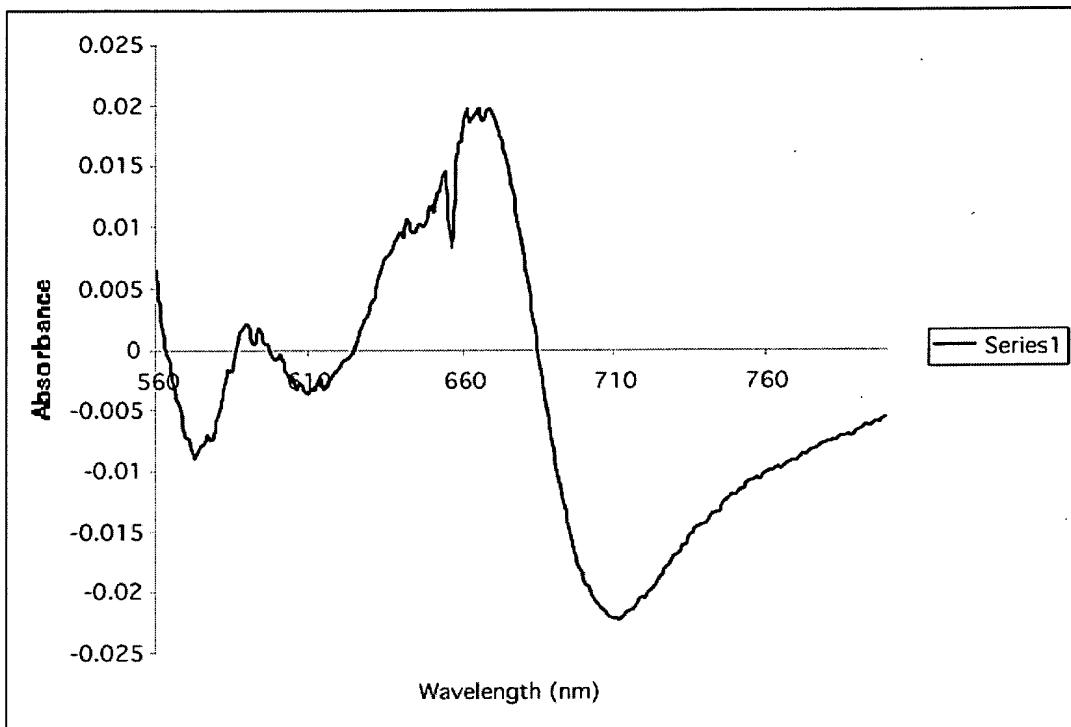


Fig. 15

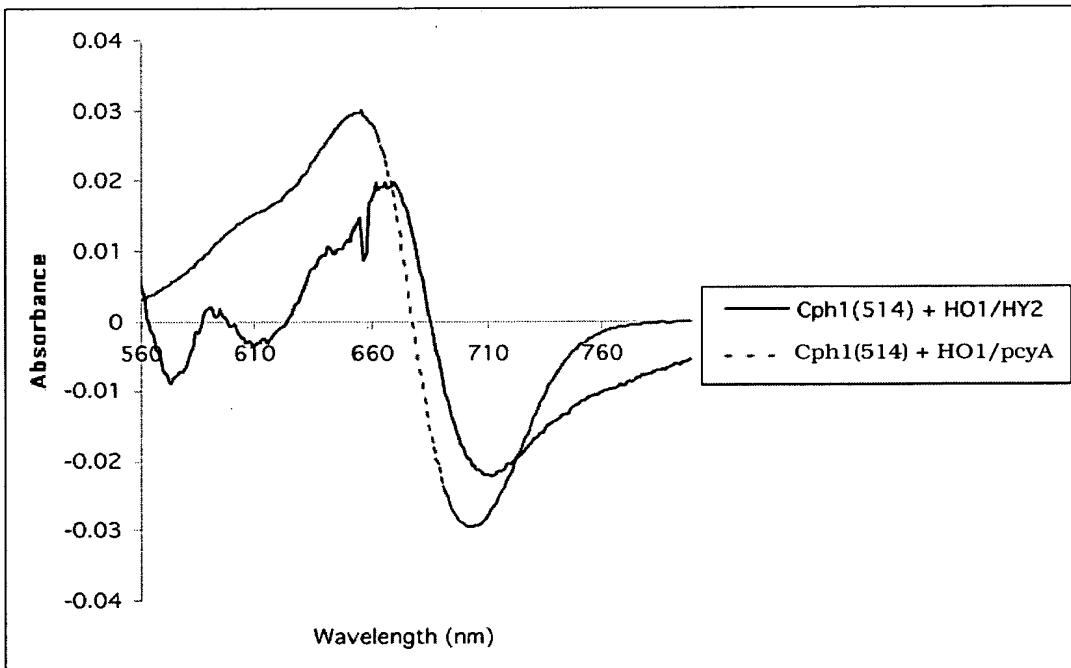


Fig. 16